

SEQUENCE LISTING

LEIPER, James WHITLEY, Guy CHARLES, Ian

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ctc tac gtg ggc gtg ctg ggc agc aag ctg ggg ctg cag gtg gtg gag Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu 50 55 60										
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		agg Arg														336
		aat Asn 115														384
		gtt Val														432
		aat Asn		_		_	_		-	_	-					480
	_	gtc Val						-	-		_		_	-		528
	_	agc Ser	_	_				_						_	_	576
		cag Gln 195														624
		aaa Lys														672
		atc Ile						-	_	_		_		_	_	720
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Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln 35 40

Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu 50 55 60

Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val 65 70 75 80

Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro 85 90 95

Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu 100 105 110

Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly 115 120 125

Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys 130 135 140

Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp 145 150 155 160

Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser 165 170 175

Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu 180 185 190

Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg 195 200 205

Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr 210 220

Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu 225 230 235 240

Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met 245

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tcc ctg acc ctc cca gat gac gca gct gct gac tgt ctc ttt ctt cgt 210																	
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Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr 245 ctg gta cct gtg tcc tca gaa ctg gag aaa gct ggc gcc ggg ctc Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu 260 agc tcc ctc tgc ttg gtg ctc agc acc cgc ccc cac agc tga 858 ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser 285 <210> 4 <211> 285 <2212> PRT <213> Homo sapiens <4400> 4 Met Gly Thr Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly Ala Gly 20 Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu Gly Gly Gly Leu Gly Val Leu Gly Gly Val Leu Gly Gly Leu Gly Leu Gly Leu Gly Leu Gly Val Leu Gly Gly Val Leu Gly Gly Leu Gly Gly Thr Asp Gly Gly Gly Fly Asp Glu Phe Phe Val Gly Leu Ser Lys Trp Thr 130 Asp His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala	Pro	Gly				Val					Leu					Gly	720
Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu 270 agc tcc ctc tgc ttg gtg ctc agc aca cgc ccc cac agc tga 858 Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser 275	gat Asp	ctg Leu	ccc Pro	aac Asn	Ser	cag Gln	gag Glu	gca Ala	ctg Leu	Gln	aag Lys	ctc Leu	tct Ser	gat Asp	Val	acc Thr	768
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Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro 50 Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val 70 For Rev Gln Arg Pro Trp Ser Pro Ala Arg Ser Rev	Arg	Gly	Val		Glu	Ser	Leu	Ala		Gly	Glu	Gly	Ala		Ala	Gly	
Fro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val 75 Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg 95 Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu 110 Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp 125 Val Leu Phe Thr Gly Arg Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala	Leu	Pro		Leu	Asp	Leu	Ala		Ala	Gln	Arg	Glu		Gly	Val	Leu	
70 75 80 Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg 95 Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu 110 Gly Leu 100 Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp 115 Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr 130 Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala	Gly	-	Lys	Leu	Arg	Gln	_	Leu	Gly	Leu	Gln		Leu	Glu	Leu	Pro	
Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu 100 Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp 115 Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr 130 Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala		Glu	Glu	Ser	Leu		Leu	Gly	Pro	Leu		Gly	Asp	Thr	Ala		
Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp 115 Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr 130 Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala	Ile	Gln	Gly	Asp		Ala	Leu	Ile	Thr		Pro	Trp	Ser	Pro		Arg	
Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr 130 135 140 Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala	Arg	Pro	Glu		Asp	Gly	Val	Arg		Ala	Leu	Gln	qaA		Gly	Leu	
130 135 140 Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala	Arg	Ile		Glu	Ile	Gly	Asp		Asn	Ala	Thr	Leu		Gly	Thr	Asp	
	Val		Phe	Thr	Gly	Arg		Phe	Phe	Val	Gly		Ser	Lys	Trp	Thr	
			Arg	Gly	Ala		Ile	Val	Ala	Asp		Phe	Arg	Asp	Phe		

Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys 170 165 Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala 185 Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala 200 Ser Leu Thr Leu Pro Asp Asp Ala Ala Asp Cys Leu Phe Leu Arg Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly 230 235 Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr 245 250 Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu 265 Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser 280 <210> 777 <211> <212> DNA <213> S. coelicolor <220> <221> CDS <222> (1)..(777)<400> 5 gtg ccc agc aag aag gcc ctg gtc cgc cgc ccc agc ccc agg ctc gcc 48 Val Pro Ser Lys Lys Ala Leu Val Arg Arg Pro Ser Pro Arg Leu Ala 96 gaa gga ctg gtg aca cac gtc gag cgg gag cag gtc gat cac ggc ctg Glu Gly Leu Val Thr His Val Glu Arg Glu Gln Val Asp His Gly Leu 20 25 gcc ctc gaa cag tgg gac gcc tac gtc gag gcc ctc gga gca cac ggc 144 Ala Leu Glu Gln Trp Asp Ala Tyr Val Glu Ala Leu Gly Ala His Gly 192 tgg gag act ctg gag gtg gac ccg gcc gag tac tgt ccg gac tcg gtc Trp Glu Thr Leu Glu Val Asp Pro Ala Glu Tyr Cys Pro Asp Ser Val ttc gtc gag gac gcc gtc gtg ttc cgc aac gtc gcg ctg atc acg 240 Phe Val Glu Asp Ala Val Val Val Phe Arg Asn Val Ala Leu Ile Thr 70 75 65 cgg ccc ggc gcc gag tcg cgc gcg gcg gag acg gcc ggc gtc gag gag 288 Arg Pro Gly Ala Glu Ser Arg Arg Ala Glu Thr Ala Gly Val Glu Glu

	85	90	95
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		g atc ggc gac acg atc s Ile Gly Asp Thr Ile 125	
		c ggt gtc cag cag ttg a Gly Val Gln Gln Leu 140	
		c gtc gcc gtg ccc gtg l Val Ala Val Pro Val 155	-
		c gcg ctg ccg gac ggg r Ala Leu Pro Asp Gly 170	
		g ccc tcg ctg ttc ccc l Pro Ser Leu Phe Pro 5 190	
		g cac gtg gtg ctg ctc a His Val Val Leu Leu 205	
		g ccc aag acg gcg gag a Pro Lys Thr Ala Glu 220	=
		c gtc gac atc ggg gag u Val Asp Ile Gly Glu 235	
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							cgc Arg 40									144	
		_	-	_	_	_	gaa Glu	~			_	_			~	192	
	_	_			~		tcg Ser	_	-	-				-		240	
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cag Gln							gtc Val									336	
gtg Val	•	~		_		_	_	_		_						384	
							gag Glu									432	
ctg Leu 145																480	
ctg Leu														-	_	528	
gcc Ala																576	
atc Ile																624	
aac Asn																672	
atc Ile 225	gcc Ala	cgc Arg	ctc Leu	ggc Gly	tac Tyr 230	cgg Arg	gtg Val	atc Ile	gag Glu	gtg Val 235	gac Asp	acc Thr	tcc Ser	gaa Glu	tat Tyr 240	720	

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Glu Gln His Asn Ala Tyr Ile Arg Ala Leu Gln Thr Cys Asp Val Asp $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Ile Thr Leu Leu Pro Pro Asp Glu Arg Phe Pro Asp Ser Val Phe Val 50 55 60

Glu Asp Pro Val Leu Cys Thr Ser Arg Cys Ala Ile Ile Thr Arg Pro 65 70 75 80

Gly Ala Glu Ser Arg Arg Gly Glu Thr Glu Ile Ile Glu Glu Thr Val\$85\$ 90 95

Gln Arg Phe Tyr Pro Gly Lys Val Glu Arg Ile Glu Ala Pro Gly Thr 100 105 110

Val Glu Ala Gly Asp Ile Met Met Val Gly Asp His Phe Tyr Ile Gly 115 120 125

Glu Ser Ala Arg Thr Asn Ala Glu Gly Ala Arg Gln Met Ile Ala Ile 130 135 140

Leu Glu Lys His Gly Leu Ser Gly Ser Val Val Arg Leu Glu Lys Val 145 150 155 160

Leu His Leu Lys Thr Gly Leu Ala Tyr Leu Glu His Asn Asn Leu Leu 165 170 175

Ala Ala Gly Glu Phe Val Ser Lys Pro Glu Phe Gln Asp Phe Asn Ile 180 185 190

Ile Glu Ile Pro Glu Glu Glu Ser Tyr Ala Ala Asn Cys Ile Trp Val 195 200 205

Asn Glu Arg Val Ile Met Pro Ala Gly Tyr Pro Arg Thr Arg Glu Lys 210 215 220

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Arg Lys Ile Asp Gly Gly Val Ser Cys Met Ser Leu Arg Phe

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	cg agc ro Ser 35														14	4
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	gc atc ly Ile														24	0
	ac ccg sn Pro														28	8
	gc gtc er Val														33	6
	tg gag eu Glu 115														38	4
Ala As	ac gac sp Asp 30	-		-	_	_		_				_	_		43	2
	ag tac lu Tyr	_				-		_	_	_	-	_	-		48	0
	ag ttc ln Phe														52	8
ctg aa	ac ccg	atg	tac	tgg	ccg	gcg	cga	cga	cag	gaa	acc	ctg	ctg	acc	57	6

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	tgg Trp 210															672	
	ggc Gly	-		_	_						_	-			_	720	
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	gcc Ala															816	
	cgc Arg															864	
_	ctg Leu 290			_		-			_	-						912	
_	ctg Leu	-		-	_	_	-				-			_	_	960	
	gag Glu															1008	
	ctg Leu		_	_		_				-						1056	
	caa Gln															1104	
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Asn Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu 50 55 60

Arg Gly Ile Asp Val Leu Glu Met His Asn Leu Leu Thr Glu Thr Ile 70 75 80

Gln Asn Pro Glu Ala Leu Lys Trp Ile Leu Asp Arg Lys Ile Thr Ala 85 90 95

Asp Ser Val Gly Leu Gly Leu Thr Ser Glu Leu Arg Ser Trp Leu Glu
100 105 110

Ser Leu Glu Pro Arg Lys Leu Ala Glu Tyr Leu Ile Gly Gly Val Ala 115 120 125

Ala Asp Asp Leu Pro Ala Ser Glu Gly Ala Asn Ile Leu Lys Met Tyr 130 135 140

Arg Glu Tyr Leu Gly His Ser Ser Phe Leu Leu Pro Pro Leu Pro Asn 145 150 155 160

Thr Gln Phe Thr Arg Asp Thr Thr Cys Trp Ile Tyr Gly Gly Val Thr
165 170 175

Leu Asn Pro Met Tyr Trp Pro Ala Arg Arg Gln Glu Thr Leu Leu Thr
180 185 190

Thr Ala Ile Tyr Lys Phe His Pro Glu Phe Ala Asn Ala Glu Phe Glu
195 200 205

Ile Trp Tyr Gly Asp Pro Asp Lys Asp His Gly Ser Ser Thr Leu Glu 210 215 220

Gly Gly Asp Val Met Pro Ile Gly Asn Gly Val Val Leu Ile Gly Met 225 230 235 240

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Phe Ala Lys Gly Ala Ala Glu Arg Val Ile Val Ala Gly Leu Pro Lys 260 265 270	
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Asp Leu Val Thr Val Phe Pro Glu Val Val Lys Glu Ile Val Pro Phe 290 295 300	
Ser Leu Arg Pro Asp Pro Ser Ser Pro Tyr Gly Met Asn Ile Arg Arg 305 310 315 320	
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Lys Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala Glu Arg 340 345 350	
Glu Gln Trp Asp Asp Gly Asn Asn Val Val Cys Leu Glu Pro Gly Val 355 360 365	
Val Val Gly Tyr Asp Arg Asn Thr Tyr Thr Asn Thr Leu Leu Arg Lys 370 375 380	
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ggttctatca	cctggacacc	gcgctggccg	tgctcgacga	ccacacgatc	gcctactacc	660
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tggtcggcag	tgccgacgcg	ttcgtgttcg	gactcaacgc	cgtctctgac	ggtctgaacg	780
tagtgcttcc	ggtcgcggcc	atgggttttg	cggcgcagtt	acgcgcagcc	ggcttcgagc	840
cggtcggtgt	cgatctgtcc	gagctgctca	agggcggcgg	ttccgtcaag	tgctgcacgc	900
tggagataca	cccatgacaa	atctcgcgga	tgccactcag	gccactatgg	cactggtcga	960
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<211> 305

<212> PRT

<213> M. tuberculosis

<400> 12

Asn Val Ser Met Glu Asn Thr Gln Arg Pro Ser Phe Asp Cys Glu Ile 1 5 10 15

Arg Ala Lys Tyr Arg Trp Phe Met Thr Asp Ser Tyr Val Ala Ala Ala 20 25 30

Arg Leu Gly Ser Pro Ala Arg Arg Thr Pro Arg Thr Arg Arg Tyr Ala 35 40 45

Met Thr Pro Pro Ala Phe Phe Ala Val Ala Tyr Ala Ile Asn Pro Trp 50 55 60

Met Asp Val Thr Ala Pro Val Asp Val Gln Val Ala Gln Ala Gln Trp 65 70 75 80

Glu His Leu His Gln Thr Tyr Leu Arg Leu Gly His Ser Val Asp Leu 85 90 95

Ile Glu Pro Ile Ser Gly Leu Pro Asp Met Val Tyr Thr Ala Asn Gly
100 105 110

Gly Phe Ile Ala His Asp Ile Ala Val Val Ala Arg Phe Arg Phe Pro 115 120 125

Glu Arg Ala Gly Glu Ser Arg Ala Tyr Ala Ser Trp Met Ser Ser Val $130 \\ 135 \\ 140$

Gly Tyr Arg Pro Val Thr Thr Arg His Val Asn Glu Gly Gln Gly Asp 145 150 155 160

Leu Leu Met Val Gly Glu Arg Val Leu Ala Gly Tyr Gly Phe Arg Thr

165 170 175

Asp Gln Arg Ala His Ala Glu Ile Ala Ala Val Leu Gly Leu Pro Val 180 185 190

Val Ser Leu Glu Leu Val Asp Pro Arg Phe Tyr His Leu Asp Thr Ala 195 200 205

Leu Ala Val Leu Asp Asp His Thr Ile Ala Tyr Tyr Pro Pro Ala Phe 210 215 220

Ser Thr Ala Ala Gln Glu Gln Leu Ser Ala Leu Phe Pro Asp Ala Ile 225 230 235 240

Val Val Gly Ser Ala Asp Ala Phe Val Phe Gly Leu Asn Ala Val Ser $245 \hspace{1.5cm} 250 \hspace{1.5cm} 255$

Asp Gly Leu Asn Val Val Leu Pro Val Ala Ala Met Gly Phe Ala Ala 260 265 270

Gln Leu Arg Ala Ala Gly Phe Glu Pro Val Gly Val Asp Leu Ser Glu 275 280 285

Leu Leu Lys Gly Gly Gly Ser Val Lys Cys Cys Thr Leu Glu Ile His 290 295 300

Pro 305

<210> 13

<211> 282

<212> PRT

<213> M. tuberculosis

<400> 13

Met Thr Asp Ser Tyr Val Ala Ala Ala Arg Leu Gly Ser Pro Ala Arg 1 5 10 15

Arg Thr Pro Arg Thr Arg Arg Tyr Ala Met Thr Pro Pro Ala Phe Phe 20 25 30

Ala Val Ala Tyr Ala Ile Asn Pro Trp Met Asp Val Thr Ala Pro Val
35 40 45

Asp Val Gln Val Ala Gln Ala Gln Trp Glu His Leu His Gln Thr Tyr
50 55 60

Leu Arg Leu Gly His Ser Val Asp Leu Ile Glu Pro Ile Ser Gly Leu 65 70 75 80

Pro Asp Met Val Tyr Thr Ala Asn Gly Gly Phe Ile Ala His Asp Ile
85 90 95

Ala Val Val Ala Arg Phe Arg Phe Pro Glu Arg Ala Gly Glu Ser Arg
100 105 110

Ala Tyr Ala Ser Trp Met Ser Ser Val Gly Tyr Arg Pro Val Thr Thr

115 120 125

Arg His Val Asn Glu Gly Gln Gly Asp Leu Leu Met Val Gly Glu Arg 130 135 140

- Val Leu Ala Gly Tyr Gly Phe Arg Thr Asp Gln Arg Ala His Ala Glu 145 150 155 160
- Ile Ala Ala Val Leu Gly Leu Pro Val Val Ser Leu Glu Leu Val Asp 165 170 175
- Pro Arg Phe Tyr His Leu Asp Thr Ala Leu Ala Val Leu Asp Asp His 180 185 190
- Thr Ile Ala Tyr Tyr Pro Pro Ala Phe Ser Thr Ala Ala Gln Glu Gln 195 200 205
- Leu Ser Ala Leu Phe Pro Asp Ala Ile Val Val Gly Ser Ala Asp Ala 210 215 220
- Phe Val Phe Gly Leu Asn Ala Val Ser Asp Gly Leu Asn Val Val Leu 225 230 230 235
- Pro Val Ala Ala Met Gly Phe Ala Ala Gln Leu Arg Ala Ala Gly Phe 245 250 255
- Glu Pro Val Gly Val Asp Leu Ser Glu Leu Leu Lys Gly Gly Gly Ser 260 265 270
- Val Lys Cys Cys Thr Leu Glu Ile His Pro 275 280
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- <211> 285
- <212> PRT
- <213> Rattus norvegicus
- <400> 14
- Met Ala Gly Leu Ser His Pro Ser Val Phe Gly Arg Ala Thr His Ala 1 5 10 15
- Val Val Arg Ala Pro Pro Glu Ser Leu Cys Arg His Ala Leu Arg Arg 20 25 30
- Ser Gln Gly Glu Glu Val Asp Phe Ala Arg Ala Glu Arg Gln His Gln 55 40 45
- Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Gln 50 55
- Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val 65 70 75 80
- Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro 85 90 95

Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu 100 105 110

Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly 115 120 125

Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys 130 135 140

Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp 145 150 155 160

Tyr Ala Val Ser Thr Val Pro Val Ala Asp Ser Leu His Leu Lys Ser 165 170 175

Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
180 185 190

Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg 195 200 205

Tyr Asp Lys Leu Thr Val Pro Asp Asp Met Ala Ala Asn Cys Ile Tyr 210 215 220

Leu Asn Ile Pro Ser Lys Gly His Val Leu Leu His Arg Thr Pro Glu 225 230 235 240

Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Leu 245 250 255

Leu Ile Pro Val Ser Asn Ser Glu Met Glu Lys Val Asp Gly Leu Leu 260 265 270

Thr Cys Cys Ser Val Phe Ile Asn Lys Lys Thr Asp Ser 275 280 285

<210> 15

<211> 72

<212> PRT

<213> Homo sapiens

<400> 15

Asn Ala Thr Leu Asp Gly Gly Asp Val Leu Phe Thr Gly Arg Glu Phe 1 5 10 15

Phe Val Gly Leu Ser Lys Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu 20 25 30

Ala Asp Thr Phe Lys Asp Tyr Ala Val Ser Thr Val Pro Val Ala Asp 35 40 45

Gly Leu His Leu Lys Ser Phe Cys Ser Met Ala Gly Pro Asn Leu Ile 50 55 60

Ala Ile Gly Ser Ser Glu Ser Ala 65 70

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Phe Val Gly Leu Ser Lys Trp Thr Asn His Arg Gly Ala Glu Ile Val
Ala Asp Thr Phe Arg Asp Phe Ala Val Ser Thr Val Pro Val Ser Gly
Pro Ser His Leu Arg Gly Leu Cys Gly Met Gly Gly Pro Arg Thr Val
Val Ala Gly Ser Ser Asp Ala Ala
                    70
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<211> 80
<212> PRT
<213> Pseudomonas aeruginosa
Asn Ala Thr Leu Glu Gly Gly Asp Val Met Pro Val Gly Lys Gly Ile
                                    10
Val Leu Ile Gly Met Gly Glu Arg Thr Ser Arg His Ala Ile Gly Gln
 Leu Ala Cln Asn Leu Phe Glu Lys Gly Ala Ala Glu Lys Ile Ile Val
         35
 Ala Gly Leu Pro Lys Ser Arg Ala Ala Met His Leu Asp Thr Val Phe
                         55
 Ser Phe Cys Asp Arg Asp Leu Val Thr Val Phe Pro Glu Val Val Lys
                     70
 65
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 <212> PRT
 <213> P. aeruginosa
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 Leu Arg Lys Val Met Val Cys Ser Pro Gly Leu Ala His Gln Arg Leu
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Thr Pro Ser Asn Cys Asp Glu Leu Leu Phe Asp Asp Val Ile Trp Val

Asn Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu 55 Arg Gly Ile Asp Val Leu Glu Met His Asn Leu Leu Thr Glu Thr Ile 75 Gln Asn Pro Glu Ala Leu Lys Trp Ile Leu Asp Arg Lys Ile Thr Ala 90 Asp Ser Val Gly Leu Gly Leu Thr Ser Glu Leu Arg Ser Trp Leu Glu 105 Ser Leu Glu Pro Arg Lys Leu Ala Glu Tyr Leu Ile Gly Gly Val Ala Ala Asp Asp Leu Pro Ala Ser Glu Gly Ala Asn Ile Leu Lys Met Tyr Arg Glu Tyr Leu Gly His Ser Ser Phe Leu Leu Pro Pro Leu Pro Asn 150 Thr Gln Phe Thr Arg Asp Thr Thr Cys Trp Ile Tyr Gly Gly Val Thr 170 Leu Asn Pro Met Tyr Trp Pro Ala Arg Arg Gln Glu Thr Leu Leu Thr 185 180 Thr Ala Ile Tyr Lys Phe His Pro Glu Phe Ala Asn Ala Glu Phe Glu 200 Ile Trp Tyr Gly Asp Pro Asp Lys Asp His Gly Ser Ser Thr Leu Glu 220 215 Gly Gly Asp Val Met Pro Ile Gly Asn Gly Val Val Leu Ile Gly Met 230 Gly Glu Arg Ser Ser Arg Gln Ala Ile Gly Gln Val Ala Gln Ser Leu 250 Phe Ala Lys Gly Ala Ala Glu Arg Val Ile Val Ala Gly Leu Pro Lys 260 Ser Arg Ala Ala Met His Leu Asp Thr Val Phe Ser Phe Cys Asp Arg Asp Leu Val Thr Val Phe Pro Glu Val Val Lys Glu Ile Val Pro Phe 295 Ser Leu Arg Pro Asp Pro Ser Ser Pro Tyr Gly Met Asn Ile Arg Arg 315 310 305 Glu Glu Lys Thr Phe Leu Glu Val Val Ala Glu Ser Leu Gly Leu Lys 335 330

Lys Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala Glu Arg 345

Glu Gln Trp Asp 355 <210> 19 <211> 202 <212> PRT <213> P. aeruginosa <400> 19 Met Phe Lys His Ile Ile Ala Arg Thr Pro Ala Arg Ser Leu Val Asp Gly Leu Thr Ser Ser His Leu Gly Lys Pro Asp Tyr Ala Lys Ala Leu Glu Gln His Asn Ala Tyr Ile Arg Ala Leu Gln Thr Cys Asp Val Asp Ile Thr Leu Leu Pro Pro Asp Glu Arg Phe Pro Asp Ser Val Phe Val Glu Asp Pro Val Leu Cys Thr Ser Arg Cys Ala Ile Ile Thr Arg Pro Gly Ala Glu Ser Arg Arg Gly Glu Thr Glu Ile Ile Glu Glu Thr Val 85 90 Gln Arg Phe Tyr Pro Gly Lys Val Glu Arg Ile Glu Ala Pro Gly Thr Val Glu Ala Gly Asp Ile Met Met Val Gly Asp His Phe Tyr Ile Gly 120 Glu Ser Ala Arg Thr Asn Ala Glu Gly Ala Arg Gln Met Ile Ala Ile Leu Glu Lys His Gly Leu Ser Gly Ser Val Val Arg Leu Glu Lys Val 150 155 Leu His Leu Lys Thr Gly Leu Ala Tyr Leu Glu His Asn Asn Leu Leu 165 170 Ala Ala Gly Glu Phe Val Ser Lys Pro Glu Phe Gln Asp Phe Asn Ile 190 185 Ile Glu Ile Pro Glu Glu Glu Ser Tyr Ala 200 <210> 20 <211> 21 <212> DNA <213> artificial sequence <220> <223> PCR primer homologous to nucleotides 303-324 of human DDAHI

<400> 20

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gcttctttca tcatgtcaac c
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cccaacaaag ggcacgtctt g
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upstream EcoRI site
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downstream XbaI site
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<212> DNA
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<223> PCR primer homologous to nucleotides 3379-3402 of human eNOS
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caaccaacgt cctgcagacc gtgc
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<223> PCR primer homologous to nucleotides 3690-3667 of human eNOS
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                                                                     24
ggcggacctg agtcgggcag ccgc
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<212> DNA
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<223> 5'/3' RACE oligo d(T) anchor primer
<400> 34
gaccacgcgt atcgatgtcg acttttttt tttttttv
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<223> 5'/3' RACE anchor primer
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<210> 36
<211> 29
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<223> PCR primer homologous to nucleotides -9-20 of S. coelicolor DDAH encoding
an upstream EcoRI site
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gatcgaattg tgcccagcaa gaaggcctg
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<211> 29
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<223> PCR primer homologous to nucleotides 732-751 of S. coelicolor DDAH
encoding a downstream XbaI site
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gatctctaga tcagtcgtac agctcgcgc
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<211> 25
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<223> PCR primer homologous to nucleotides 1-19 of P. aeruginosa DDAH encoding
an upstream EcoRI site
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<210> 39
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<212> DNA
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<223> PCR primer homologous to nucleotides 782-768 of P. aeruginosa DDAH
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encoding an upstream EcoRI site
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